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Run
                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                          seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein search, using sw model
                                                                  SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
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225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PEDPQRRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQ 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                sp_bacteria:*
                                                                                                                                                                             sp_organelle:*
                                                                                                                                                                                                               sp_mammal:*
                                                                                                                                                                                                                              sp_invertebrate: *
                                                                                                                                                                                                                                                                                                 sp_archea:*
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sp_virus:*
                                                                        sp_unclassified:*
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15.642 Million cell updates/sec
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## SUMMARIES

19	18	17	16	15	14	, 143	12	11	10	9	8	7	o	. <b>ഗ</b>	4	ω	2	<u></u>	Result No.
77.5	78	79	79	80	81	81	81	81.5	82	82	83	83	84.5	112	112	114	117.5	119	Score
34.4	34.7	35.1	35.1	35.6	36.0	36.0	36.0	36.2	36.4	36.4	36.9	36.9	37.6	49.8	49.8	50.7	52.2	52.9	Query Match Length DB
652	648	278	277	1457	2678	821	663	2123	339	154	1703	1403	1556	666	625	666	593	525	ength 1
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015410	Q9TXB8	Q9M4M1	Q9M4L8	044011	Q9NDS4	Q9W3A1	Q9W352	Q9U9S7	Q16845	Q9UC02	Q9VGP8	Q9U6A2	Q9U6A1	Q9SPL4	Q9SPL3	Q9SPL5	Q9SEW4	Q43358	ID
015410 homo sapien	Q9txb8 dictyosteli	Q9m4m1 triticum ae	Q9m4l8 triticum ae	044011 dictyosteli	Q9nds4 dictyosteli	_	Q9w352 drosophila	Q9u9s7 dictyosteli	_	_	Q9vgp8 drosophila	Q9u6a2 drosophila	Q9u6al drosophila	Q9spl4 macadamia i	Q9spl3 macadamia i	Q9sp15 macadamia i	Q9sew4 juglans reg	Q43358 theobroma c	Description

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45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20
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33.3	33.3	٠	ω.	w ·	ω.	33.3	33.6	33.6	33.6	33.6	33.8	33.8	33.8	33.8	33.8	33.8	34.0	34.0	34.0	34.0	34.2	34.2	34.4	34.4	34.4
1457	1023	910	910	900	709	517	445	438	386	63	1038	838	600	572	276	276	2074	393	388	388	1761	425	2212	2023	2023
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Q9VT35	Q9VSB0	088704	054899	Q9VK09	Q9N4R2	Q9W4E8	016511	016502	Q9W353	Q28393	060983	Q9Y0C9	Q17401	Q19594	Q9M4M0	Q9M4M2	088542	Q9ZTP0	016501	016500	077283	Q17400	Q9UHV6	Q9UND7	075557
Q9vt35 drosophila	ros	O88704 mus musculu	054899 mus musculu	Q9vk09 drosophila				016502 caenorhabdi				_		Q19594 caenorhabdi		Q9m4m2 triticum ae	O88542 mus musculu	Q9ztp0 oryza sativ				caen	Q9uhv6 homo sapien	Q9und7 homo sapien	075557 homo sapien

## ALIGNMENTS

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Q43358
  Query Match
Best Local S
Matches 18
                                                                    CHAIN
SEQUENCE
                                                                                                                                                            McHenry L., Fritz P.J.;

"Comparison of the structure and nucleotide sequences of vicilin of cocoa and cotton raise questions about vicilin evolution.";

plant Mol. Biol. 18:1173-1176(1992).

EMBL; X62625; CAA44493.1; -.

EMBL; X62626; CAA44494.1; -.

EMBL; X62626; CAA44494.1; -.

HSSP; P02853; 2PHL.

HSSP; P02853; 2PHC.

HSSP; P02853; PHC.
                                                                                                                                                                                                                                                                                                                                                                                                                   Q43358
Q43358;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-2000 (TrEMBLrel. 15,
                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Theobroma.
                                                                                                                       PRODOM; PD081059; -; 1.
                                                                                                                                    PFAM; PF00546; Seedstore_7s; 1.
                                                                                                                                                                                                                                                         MEDLINE=92288309; PubMed=1600151; McHenry L., Fritz P.J.;
                                                                                                                                                                                                                                                                                     TISSUE=LEAVES;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              Theobroma cacao (Cacao).
                                                                                                                                                                                                                                                                                                                                                                                                          VICILIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3641;
                                                                                                                                                     NTERPRO;
    Local Similarity
les 18; Conserv
                                                                                                                                                   IPR001113;
                                                                    25
525 A
    Conservative
                                                                     AA;
               52.9%;
                                                                 24 POTENTIAL.
525 VICILIN.
60798 MW; 19114CD5C248905D CRC64;
; Score 119; DB 10;
; Pred. No. 5.2e-07;
14; Mismatches 6;
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Last annotation update)
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                          Length 525;
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121

DPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRK

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                                 Query Match
Best Local S
Matches 19
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                              Q9SPL5;
Q9SPL5;
01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                                           EMBL;
                                                                                                                                                         Marcus J.P., Goulter K.C., "A family of antimicrobial globulin protein in Macadan
                                                                                                                                                Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jug r 2,
allergen.
                                                                                          SEQUENCE
                                                                                                     PFAM;
                                                                                                                                                                                           TISSUE=NUT KERNEL;
                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embr. Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. SUNLAND; TISSUE-SOMATIC EMBRYO LINE; Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A., "Identification and cloning of a cDNA encoding a vicilin-like protein, Jug r 2, from English walnut kernel (Jugians regia): a major food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidac Fagales; Juglandaceae; Juglans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TREMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-OCT-2000 (TREMBLrel. 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
Juglans regia (English walnut).
                                                                                                               INTERPRO;
                                                                                                                                                                                                                                                        Macadamia integrifolia (Macadamia nut).
                                                                                                                                                                                                                                                                           AMP2
                                                                                                                                                                                                                                                                                 VICILIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF066055; AAF18269.1; -. HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9SEW4;
01-MAY-2000
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          DPQRRYEECQQEC - -
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                                                                                                                                       amily of antimicrobial peptides is produced by pullin protein in Macadamia integrifolia karrana J. 0.00-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                           PEDPQRRYEECQQEC-RQQEERQQPQCQQRCLKRFEQEQQQ 40
= :: = : = : = : =
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                                                                                                                         AF161883; AAD54244.1; P02853; 2PHL.
                                                                                                     PF00546;
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                                 l Similarity
19; Conser
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                                                                                          666 AA;
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                                 Conservative
                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 15, Last annotation updat
                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                        Seedstore_7s; 1
AA; 78217 MW;
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RQQEERQQPQCQQRCLKRFEQEQQQ
                                            50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.2%;
                                                                                                                                                                                                                                   Embryophyta; Tracheophyta; dons; Proteaceae; Macadamia.
                               11;
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                                                                                                                                                                                                                                                                                            Last annotation update)
                               Score 114; DB 10;
Pred. No. 2.5e-06;
1; Mismatches 6
                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 117.5; DB 10; Pred. No. 8.6e-07; 4; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                       C752B884B2DF0224 CRC64;
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                                                    Length
                               Indels
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                                                                                                                                                                                                                                               Spermatophyta;
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Best Local S
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                                                                  Query Match
Best Local :
                                               Matches
                                                                                                                                                                                                                                          "A family of antimicrobial peptides is produced by p
globulin protein in Macadamia integrifolia.";
Plant J. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             globulin protein in Macadamia integrifo.
Plant J. 0:0-0(1999).
EMBL; AF161885; AAD54246.1; -.
HSSP; P02853; 2PHL.
INTERPRO; IPPOOTITY
                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                 Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Trav
Magnoliophyta; eudicotyledons; Proteaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9SPL4;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2000 (TrEMBLrel. 15,
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Q9SPL3;
01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                                                                    SEQUENCE
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                                                                                                                                                  INTERPRO; IPRO01113; PFAM; PF00546; Seeds: SEQUENCE 666 AA;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tra
Magnoliophyta; eudicotyledons; Proteaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMP2
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                                        Similarity 56.4
22; Conservative
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19; Conser
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AA; 78243 MW
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                                                              49.88;
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47.5%;
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11; Mismatches 8
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7; Mismatches
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                                                                                                                                               0ECA22F8710F8A7B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                               Tracheophyta; Spermatophyta;
eae; Macadamia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produced olia.";
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01-MAY-2000
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01-MAY-2000
01-MAY-2000
                                                                                                                                                                   Xu C., Kauffmann R.C., Zhang J., Kladny S., Carthew R.W.; "Overlapping activators and repressors delimit transcriptional response to receptor tyrosine kinase signals in the Drosophila Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF190403; AAF05703.1; -. Homeobox; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XU C., Kauffmann R.C., Zhang J., Kladny S., Carthew R.W.;
"Overlapping activators and repressors delimit transcriptional
response to receptor tyrosine kinase signals in the Drosophila
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF190405; AAF06660.1; -.
HOMBOODOX; DNA-binding; Nuclear protein.
SEQUENCE 1556 AA; 171029 MW; 6FEACFEA2D73E644 CRC64;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                  Ephydroidea;
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17; Conser
                                                                                                                                                                                                                                                                                               Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
a; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                     melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virilis
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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(TrEMBLrel. 13, Last annotation update)
TRANSCRIPTION FACTOR PROSPERO.
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Pred. No. 0.
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No. 0.026;
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ID Q5
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Best Local
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Q9UCO2 PRELIMINARY; PKT;
Q9UCO2;
O1-MAY-2000 (TrEMBLrel. 13, Created)
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Pterygota;
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DOTERNA REPORTED TO THE PROPERTY OF THE PROPER
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA Amanatides P.G., Kewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Apbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Borkova D., Betchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Port L.B., Davies B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Baryey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei X., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshlan N.V., Mobarry C., Morris J., Moshrefi A..
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Q9VGP8;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Sheier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yen J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.
                                                                                                                                                                                                                                                                                                                                                                                                                     Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

SCHENDL, AE003691; AAF54628.1; --
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EQQQQQQQQQQQQQQQQQQRRFEQEQQE 1046
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17; Conser
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Metazoa; Arthropoda; Trac
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(TrEMBLrel. 14, Last annotation update)
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Endopterygota; Diptera;
ilidae; Drosophila.
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Q16845;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA-BOUENCE-BINDING PROTEIN) (TBP).
                                                                                                                                                                                                                                                                                                                                                                                                                       KAO C., Lieberman P., Schmidt M., Zhou Q., Pei R., Berk A.J.;
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS
SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
THE POSITION OF TRANSCRIPTION INITIATION.
-i- SUBUNIT: BINDS DNA AS A MONOMER.
                                                                                                                         PRINTS; PR00686; TIFACTORIID.

PROSITE; PS00351; TFIID; 2.

Transcription regulation; DNA-binding; Nuclear protein; Duplication SEQUENCE 339 AA; 37783 MW; 98B7E26CB42B853A CRC64;
                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: THE C-TERMINAL 180 RESIDUES ARE
-CONSERVED IN ALL EUKARYOTIC TFIID.
-!- SIMILARITY: WEAK, WITH BACTERIAL POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=FIBROBLAST;
MEDLINE=90302010; PubMed=2194289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92350691; PubMed=1641350;
Hashimoto S., Fujita H., Hasegawa S., Ro
"Conserved structural motifs within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
TATA BOX-BINDING PROTEIN (FRAGMENT).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                              EMBL; M34960; AAC03409.1; HSSP; P20226; 1TGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kao C., Lieberman P., Schmidt M., Zhou "Cloning of a transcriptionally active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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Nucleic Acids Res. 20:3788-3788(1992)
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                                                                                                                                                                                                                             PFAM; PF00352; TBP; 2.
                                                                                                                                                                                                                                                    INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EDPORRYEECQOECROOEERQOPOCOORCLKRFEQEOQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                  IPR000814; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primates; Catarrhini;
                         36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 82; DB 4
Pred. No. 0.00!
14; Mismatches
                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93A5A0B5CCAFC604 CRC64;
                       No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roeder R.G., Horikos
he N-terminal domain
                         DB 4;
0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q., Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pei R., Berk A.J.;
an TATA binding factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
9;
                                                   Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 154
                                                                                                                                                                                                                                                                                                                          SIGMA-FACTORS
                                                                                                                                                                                                                                                                                                                                                                           EXTREMELY WELL
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikoshi
domain of
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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TFIID
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                        Q9W352 PRELI
Q9W352;
01-MAY-2000 (TrEM
01-MAY-2000 (TrEM
01-JUN-2000 (TrEM
CG17446 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9U9S7;
Q9U9S7;
01-MAY-2000
MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                             Eukaryota; Metazoa; Arthropo
Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; LEKULIO,
PFAM; PF00072; response_reg; 1.
PFAM; PF00271; guanylate_cyc; 1.
PRINTS; PR00344; BCTRLSENSOR.
PROSITE; PS00387; PPASE; UNKNOWN 1.
PROSITE; PS00387; PPASE; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 01-OCT-2000 (TrEMBLrel.
                                                                                                 SEQUENCE FROM N.A. STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                              1932 QQQQRQQQQQQQQQQQQQQQQQQQPQ-QQQQLQQQQQHQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF153362; HSSP; P19754; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=44689;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADENYLYL CYCLASE
                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                               CG17446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPRO00410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An adenylyl cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soderbom F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P19754; 1AWK
                                                                                                                                                                                                                                                                                                                                                                            l Similarity 43.(
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001596; -. IPR001789; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001054; -. IPR001440; -.
                                                                                                                                           Metazoa; Arthropoda; Tracheata; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyco
1, Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyosteliida;
                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anjard C.,
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                                                                                                                                                                                                                                                                                                                                                                                        36.2%;
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13,
14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13,
13,
                                                                                                                                                                                 (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Slime mold).
a; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        functions
                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                            Created)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       81.5;
No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       during
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loomis W.F.;
                                                                                                                                                                                                                                                                     663
                                                                                                                                                                                                                                                                                                                                                                                       .056;
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                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        late development
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                                                                                                                                                           Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                 Length 2123;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                      Insecta;
                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
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RESULT
Q9W3A1
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DR MERSON B.G. A. Mathia melanogaster.", Spien H.O., DR EMBL; AE003446; AAR46483.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000
01-MAY-2000
01-MAY-2000
               Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra 1 Cherry J.M., CawLey S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
                                                                                                                                                                                                                                                                                                                CG15365 PROTEIN CG15365.
                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                  STRAIN-BERKELEY;
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Ephydroidea;
                                                                                                                                                                                                                                                         Pterygota;
                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                          Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                          Q9W3A1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EDPORRYEECQQECROQEERQQPQCQQRCLKRFEQEQQQ 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00628;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.Y., Benos P.V., Berman
D., Botchan M.R., Bouck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FBgn0030121; CG17446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001965; -.
                                                                                                                                                                                                                                                       melanogaster (Fruit fly).
                                                                                                                                                                                                                                    Neoptera; Endopt
                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%;
41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76696 MW;
                                                                                                                                                                                                                                      Endopterygota; Diptera; ilidae; Drosophila.
Baxendale J.,
                                                                                                                                                                                                                                                                                                                                                 13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence
Last anno
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Pred. No. 0.02
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8573CD209AE28157 CRC64;
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J., Brokstein P., Brottier P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J., Bayraktaroglu L., B.P., Bhandari D., Bo
                                                                                                                                                                                                                                                                                                                                                   sequence update) annotation updat
Bayraktaroglu
                                                                                                                                                                                                                                                                                                                                                                                                                           821
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                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                       Brachycera; Muscomorpha
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EMBL; AB030033; BAB01489.1;
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Botchan M.R., Bouck J., Brokstein P.,
Busam D.A., Butler H., Cadieu E., Ce
                                                                                                                                                                                                                                                                                   Sutoh K.; encodes a component necessary for starvation-encodes a component necessary for starvation-vclase expression in Dictyostelium early
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MW; 7D82BFBFBEE7C
                                                     Score 81; DB
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Search completed: March
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O44011;
01-JUN-1198 (TrEMBLrel. 06, Created)
01-JUN-1198 (TrEMBLrel. 06, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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PFAM; PF00069; pkinase; 2.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

SEQUENCE 1457 AA; 167110 MW; CIFCDCE99D561856 CRC64;
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Kuspa A., Loomis W.F.;
Ruspa A., Loomis W.F.;
"Ordered yeast artificial chromosome clones representing the
Dictyostelium discoideum genome.";
Proc. Natl. Acad. Sci. U.S.A. 93:5562-5566(1996).
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Loomis W.F., Welker D., Hughes J., Maghakian D., Kuspa A.;
"Integrated maps of the chromosomes in Dictyostelium discoideum.";
Genetics 141:147-157(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuspa A., Lu S., Souza G.M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF045453; AAC02554.1; -.
HSSP; P24941; ICKP.
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